

1/33

FIGURE 1A

ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC		45
M K P Y F C R V F V F C F L I		
5 10 15		
AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG		90
R L L T G E I N G S A D H R M		
20 25 30		
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT		135
F S F H N G G V Q I S C K Y P		
35 40 45		
GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA		180
E T V Q Q L K M R L F R E R E		
50 55 60		
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG		225
V L C E L T K T K G S G N A V		
65 70 75		
TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC		270
S I K N P M L C L Y H L S N N		
80 85 90		
AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC		315
S V S F F L N N P D S S Q G S		
95 100 105		
TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA		360
Y Y F C S L S I F D P P P F Q		
110 115 120		
GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG		405
E R N L S G G Y L H I Y E S Q		
125 130 135		
CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT		450
L C C Q L K L W L P V G C A A		
140 145 150		
TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT		495
E V V V L L F G C I L I I W F		
155 160 165		
TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA		540
S K K K Y G S S V H D P N S E		
170 175 180		
TAC ATG TTC ATG GCG GCA GTC AAC ACA AAC AAA AAG TCT AGA CTT		585
Y M F M A A V N T N K K S R L		
185 190 195		
GCA GGT GTG ACC TCA		600
A G V T S		
200		

BEST AVAILABLE COPY

2/33

FIGURE 1B

mCRP1	MKPYFCRVFV FCFLIRLL-- -----TGEIN GS----ADHR MFSFHNGGVQ	39
mCD28	MT----- ---LRLFL ALNFFSVQVT ENKILVKQSP LLVVDNEVS	38
Consensus	M.....RLL..V.	
mCRP1	ISCKYPETV- -QQLKMRLFR --EREV-LCE LTKTKGSGNA VSINKPMLCL	34
mCD28	LSCRYSYNLL AKEFRASLYK GVNSDVEVCV GNGNFTYQPQ FRSNAEFNCD	38
Consensus	.SC.Y..... .L..V..C.C.	
mCRP1	YHLSNNSVSF FLNNPDSSQG SYYFCCLSIF DPPPQERNL SGGYL-HIYE	133
mCD28	GDFDNETVTF RLWNLHVNH DIYFCKIEFM YPPPYLDNER SNGTIIHIKE	138
Consensus	...N..V.F .L.N.... .YFC.... .PPP..... S.G...HI.E	
mCRP1	SQLC---CQL KL-W-LPVGC AA-FVVVLLF GCIL-IIWFS KKKY----GS	172
mCD28	KHLCHTQSSP KLFWALVVVA GVLFCYGLLV TVALCVIWTN SRRNRLLQVT	188
Consensus	.LC..... KL.W.L.V.. ...F...LL. ...L..IW..	
mCRP1	SVH-DPNSEY MFMAAVNTNK KSR-LAGVTS	200
mCD28	TMNMTPRPG LTRKPYQPYA PARDFAAYRP	218
ConsensusP..... .R..A.... .	

09/890729

PCT/US00/01871

WO 00/46240

3/33

FIGURE 2A

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC ACC AGG CAG M Q L K C P C F V S L G T R Q 5 10 15	45
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT P V W K K L H V S S G F F S G 20 25 30	90
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT L G L F L L L S S L C A A S 35 40 45	135
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC A *E T E V G A M V G S N V V L 50 55 60	180
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG S C I D P H R R H F N L S G L 65 70 75	225
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC Y V Y W Q I E N P E V S V T Y 80 85 90	270
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC Y L P Y K S P G I N V D S S Y 95 100 105	315
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC K N R G H L S L D S M K Q G N 110 115 120	360
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG F S L Y L K N V T P Q D T Q E 125 130 135	405
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG F T C R V F M N T A T E L V K 140 145 150	450
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT I L E E V V R L R V A A N F S 155 160 165	495
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA T P V I S T S D S S N P G Q E 170 175 180	540
CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC R T Y T C M S K N G Y P E P N 185 190 195	585
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT L Y W I N T D N S L I D T A 200 205 210	630
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT L Q N N T V Y L N K L G L Y D 215 220 225	675
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT V I S T L R L P W T S R G D V 230 235 240	720

4/33

FIGURE 2A (Con't)

CTG TGC TGC GTA GAG AAT GTG GCT CTC CAC CAG AAC ATC ACT AGC L C C V E N V A L H Q N I T S 245 250 255	765
ATT AGC CAG GCA GAA AGT TTC ACT GGA AAT AAC ACA AAG AAC CCA I S Q A E S F T G N N T K N P 260 265 270	810
CAG GAA ACC CAC AAT AAT GAG TTA AAA GTC CTT GTC CCC GTC CTT Q E T H N N E L K V L V P V L 275 280 285	855
GCT GTA CTG GCG GCA GCG GCA TTC GTT TCC TTC ATC ATA TAC AGA A V L A A A F V S F I I Y R 290 295 300	900
CGC ACG CGT CCC CAC CGA AGC TAT ACA GGA CCC AAG ACT GTA CAG R T R P H R S Y T G P K T V Q 305 310 315	945
CTT GAA CTT ACA GAC CAC GCC L E L T D H A 320 322	966

09/890729

PCT/US00/01871

WO 00/46240

5/33

FIGURE 2B

mB7RP1	MQLKCPFCVS LGTRQPVWKK LHVSSGFFSG LGLFLLLLS- SLCAASAETE	49
mCD80	MA--CNC--Q LMQDTPL--- LKFPCPRLI- L-LFVLLIRL SQVSSDVDEQ	41
Consensus	M....C.C... L....P.... L..... L.LF.LL... S.....	
mB7RP1	VGAMVGSNVV LSCIDPHRRH FNLSGLYVYW QIENPEVSVT YYLPYKSPGI	99
mCD80	LSKSVKDKVL LPC-RYNSPH EDESEDRIYW QKHDKVV--- --LSVIAGKL	85
ConsensusV...V. L.C.....H ...S....YW Q....V... .L.....	
mB7RP1	NVDSSYKNRG HLSLDMSMKQG NFSLYLKNVT PQDTQEFTCR VFMNTATELV	149
mCD80	KWWPEYKNR- --TL--YDNT TYSLIILGLV LSDRGTYSCV VQKKERGTYE	130
Consensus	.V...YKNR. .L..... .SL..... .D.....C. V.....	
mB7RP1	KILEEVVRLR VAANFSTPVI STSDSSNPGQ ERTYTCMSKN GYPEPNLYWI	199
mCD80	VKHIALVKLS IKADFSTPNI TESGNPSADT KRI-TCFASG GFPKPRFSWL	179
ConsensusV.L. ...A.FSTP.I ..S..... .R..TC.... G.P.P...W.	
mB7RP1	-NTTDNSLID TALQNNNTVYL NKLGLYDVIS TLRLPWTSRG DVLCCVENVA	248
mCD80	ENGRELPGIN TTISQDPSE LYTISSQLDF NTTRNHTIKC LIKYGDAHVS	229
Consensus	.N.....I. T.....T...V.	
mB7RP1	LHQNITSISQ AESFTGNNTK NPQETHNNEL KVLVPVLAVL A-AAAFVFSI	297
mCD80	EDFTWEKPPE DPPDSKNTLV LFGAGFGAVI TVVVIVVIIK CFCKHRSCFR	279
ConsensusN...1.... .V.V.V...F.	
mB7RP1	IYRRTR-PHR SYT-GPKTVQ LELETDHA	322
mCD80	RNEASRETNN SLTFGPEEAL AEQTVFL	306
ConsensusR.... S.T.GP... .E.T...	

09/890729

PCT/US00/01871

WO 00/46240

6/33

FIGURE 3A

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC M R L G S P G L L F L L F S S	45
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC L R A *D *T *Q *E K *E V R A *M V G	90
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT S D V E L S C A C P E G S R F	135
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA D L N D V Y V Y W Q T S E S K	180
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC T V V T Y H I P Q N S S L E N	225
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC V D S R Y R N R A L M S P A G	270
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC M L R G D F S L R L F N V T P	315
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG Q D E Q K F H C L V L S Q S L	360
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA G F Q E V L S V E V T L H V A	405
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC A N F S V P V V S A P H S P S	450
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC Q D E L T F T C T S I N G Y P	495
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG R P N V Y W I N K T D N S L L	540
170 175 180	
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC D Q A L Q N D T V F L N M R G	585
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC L Y D V V S V L R I A R T P S	630
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC V N I G C C I E N V L L Q Q N	675
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC L T V G S Q T G N D I G E R D	720
230 235 240	

09/890729

PCT/US00/01871

WO 00/46240

7/33

FIGURE 3A (Con't)

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT	
Y A G	864
288	

FIGURE 3B

hB7RP1	EKEVRAVGGS DVELSCACPE GSRFDLNDVY VYWQTSESKT VVTYHIPQNS	50
mB7RP1	ETEVGAMVGS NVVLSCIDPH RRHFNLSGLY VYWQIENPEV SVTYYLPYKS	50
Consensus	E.EV.AMVGS .V.LSC..P. #.F.L..Y VYWQ..... VTY..P..S	
hB7RP1	SLENVDSRYR NRALMSPAGM LRGDFSLRLF NVTPQDEQKF HCLVLSQ-SL	99
mB7RP1	PGINVDSSYK NRGHLSLDNM KQGNFSLYLK NVTPQDTQEF TCRVFMNTAT	100
Consensus	...NVDS.Y. NR...S...M ..G.FSL.L. NVTPQD.Q.F .C.V.....	
hB7RP1	GFQEVL SVEV TLHVAANFSV PVVSAPHSPS Q-DELTFTCT SINGYPRPNV	143
mB7RP1	ELVKILEEVV RLRVAANFST PVI STSDSSN PGQERTYTCM SKNGYPEPNL	150
ConsensusL...V .L.VAANFS. PV.S...S... E.T.TC. S.NGYP.PN.	
hB7RP1	YWINKTDNSL LDQALQNDTV FLNMRGLYDV VS VLRRIARTP SVNIGCCIEN	198
mB7RP1	YWINTTDNSL IDTALQNNTV YLNKLGLYDV ISTLRLPWTS RG DVLC CVEN	200
Consensus	YWIN.TDNSL .D.ALQN.TV .LN..GLYDV .S.LR...T.CC.EN	
hB7RP1	VLLQQNLTVG SQTGNDIGER DKITENPVST GEKNAATWSI LAVLCLLVVV	248
mB7RP1	VALHQNITSI SQAESFTGNN TKNPQETHNN ELKV LV--PV LAVLAAA AFV	248
Consensus	V.L.QN.T.. SQ....G.. .K....K.. .K...7... LAVL.....V	
hB7RP1	AVAIGWVCRD RCLQHSYAG	267
mB7RP1	SFI IYR--RT R-PHRSYTGP KTVQLELTDH A	276
Consensus	...I...I.R. R...SY.G. ...+.....	

9/33

Figure 4A

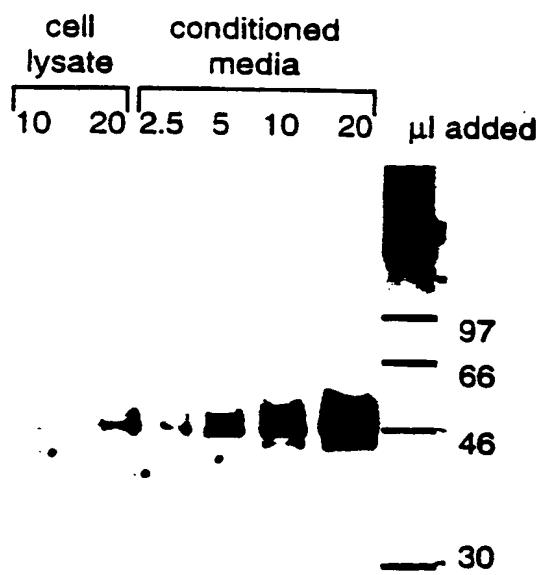
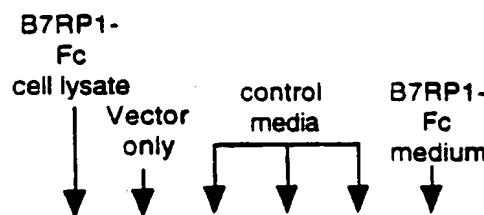


Figure 4B



PCT/US00/01871

Figure 5

Fc fusion proteins

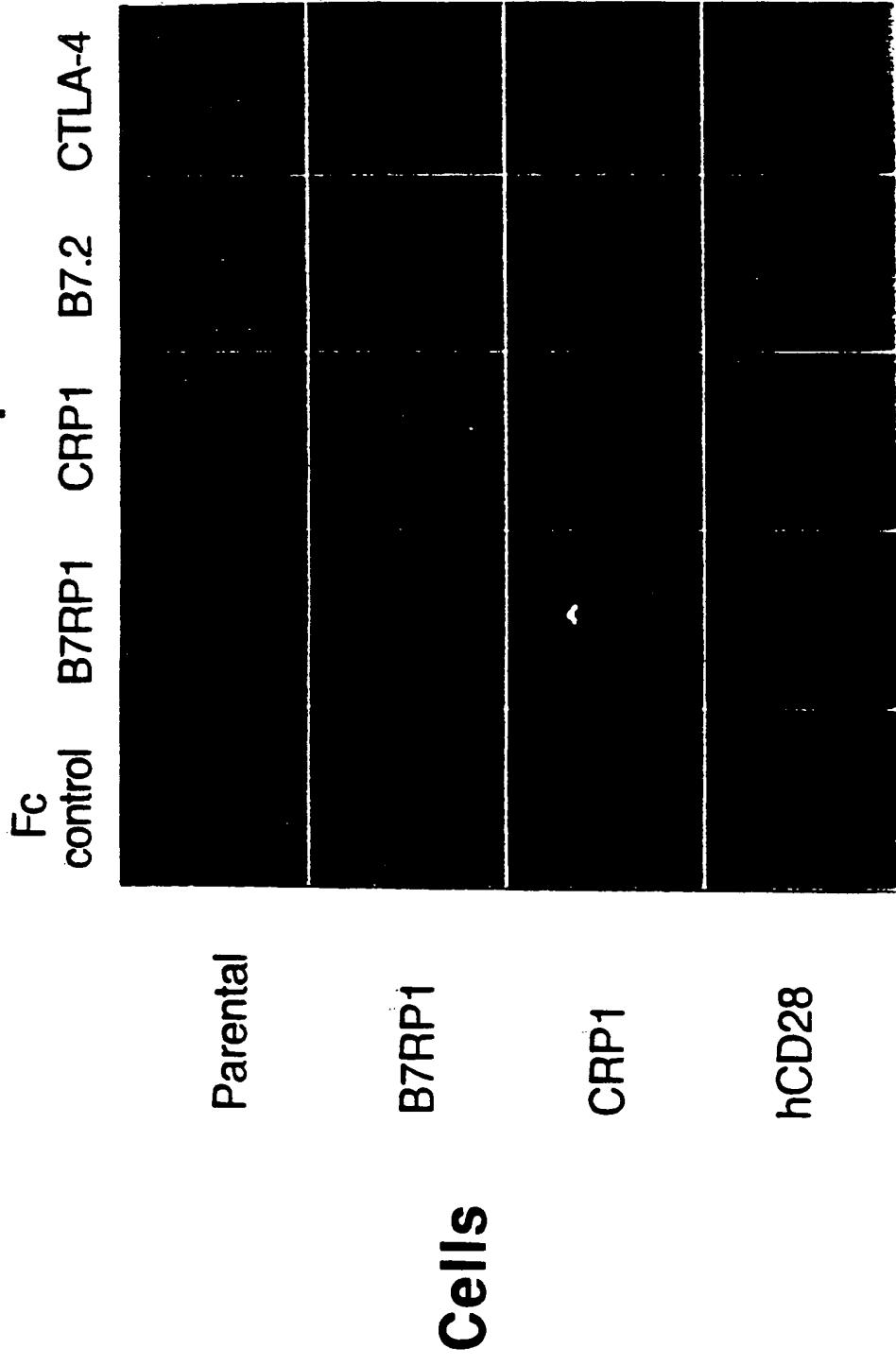


Figure 6

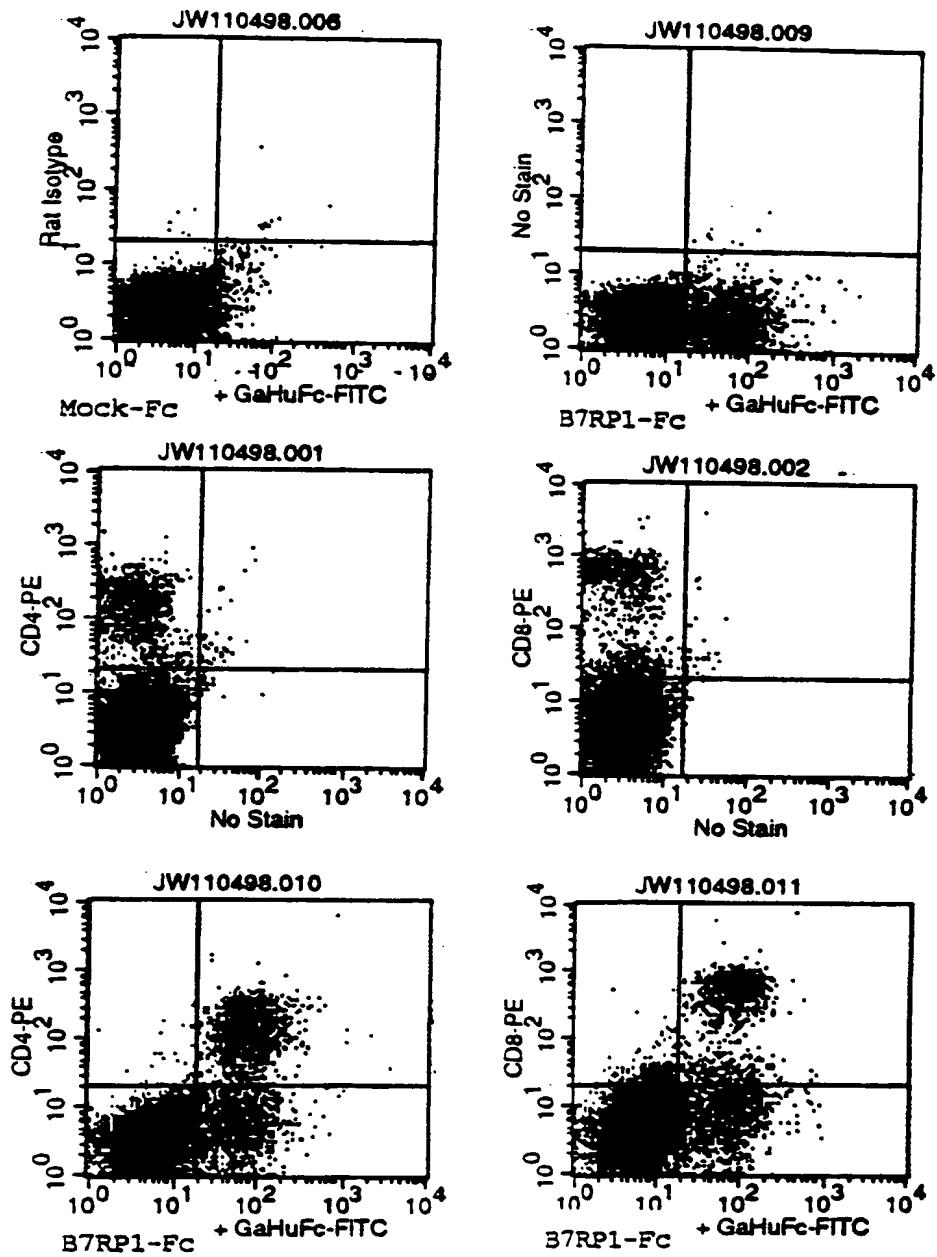


Figure 7

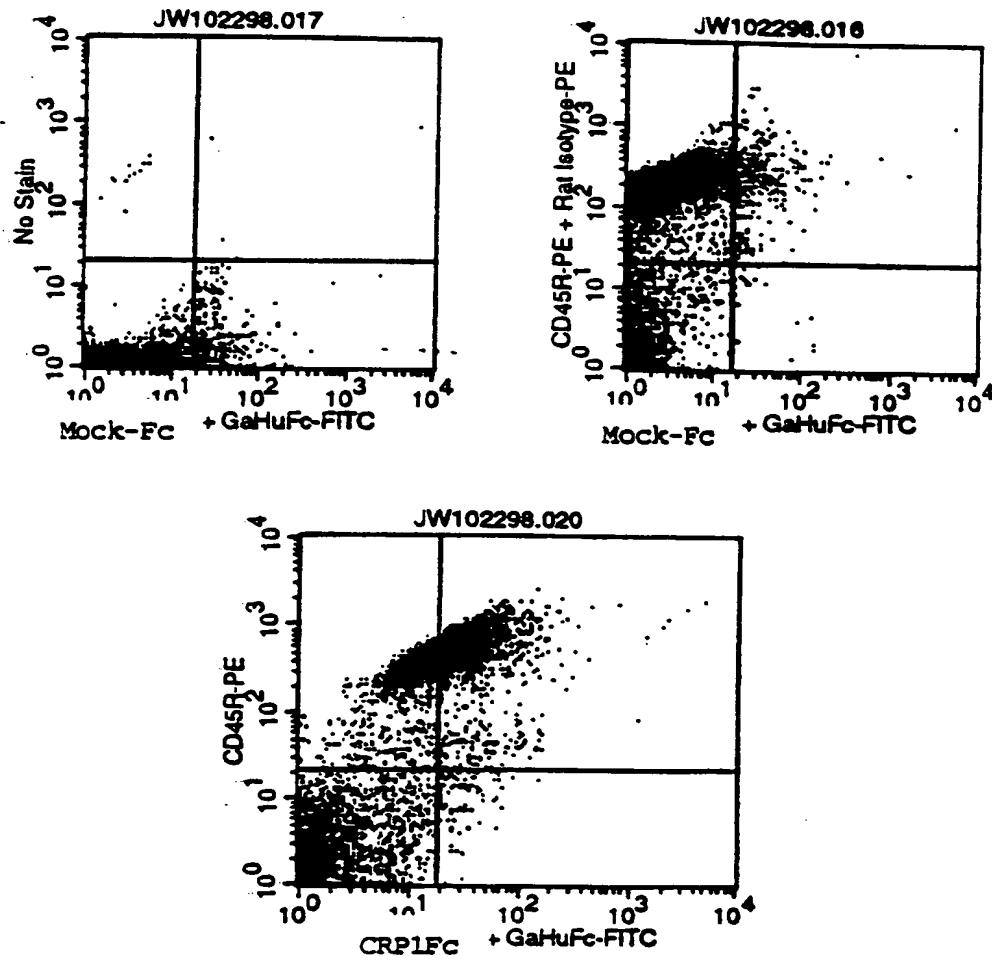


Figure 8

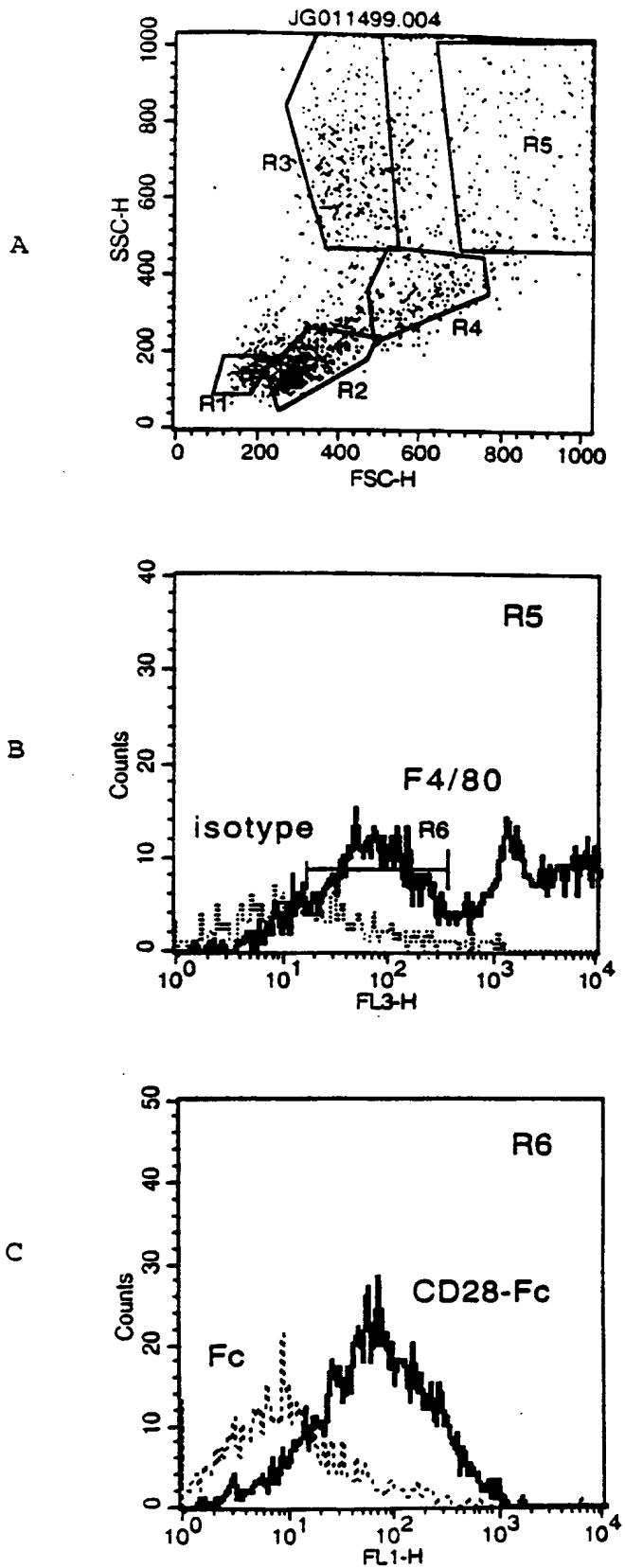


FIGURE 9

Con A stimulation of T-cells regulated
by B7RP1-Fc fusion protein

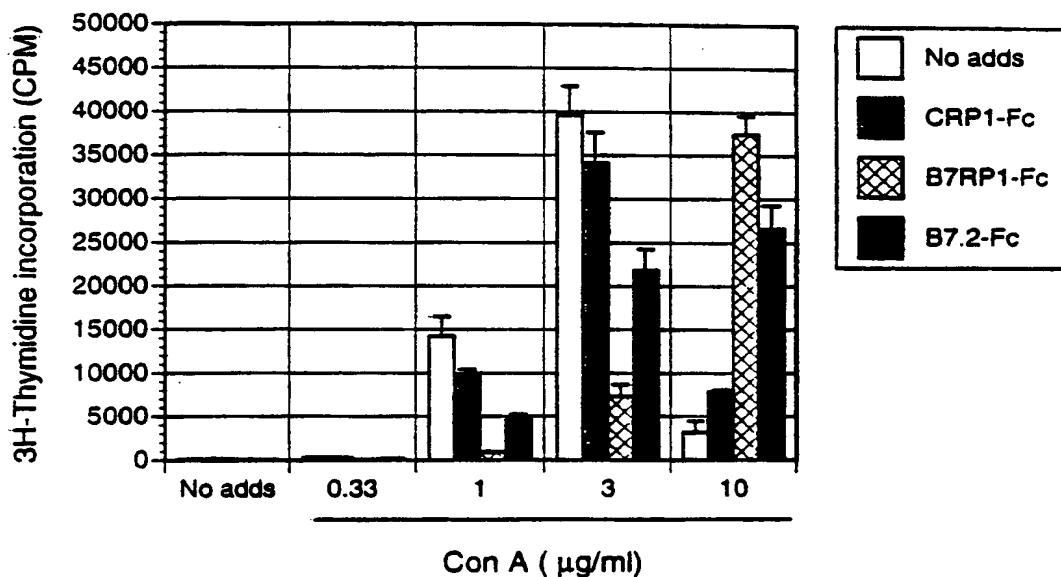


Figure 10

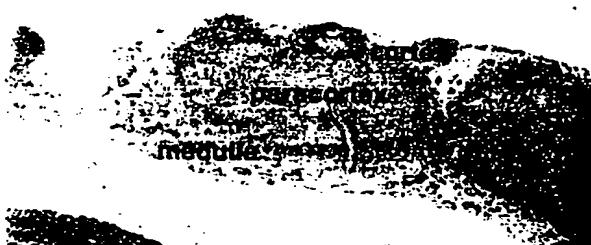
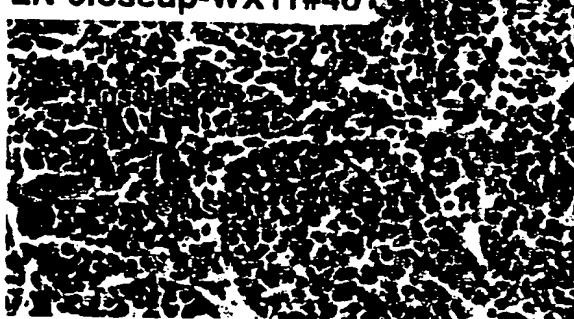
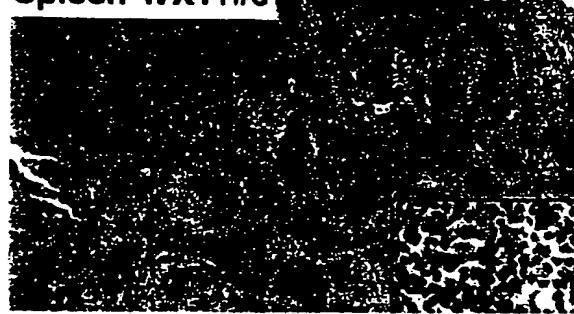
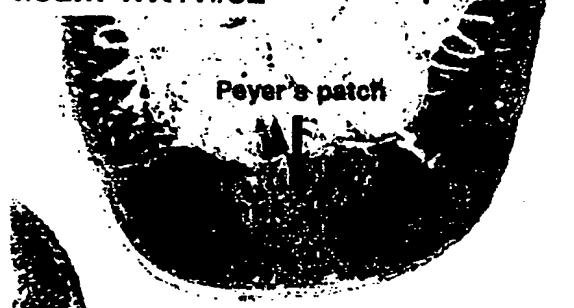
A Lymph node-control#10**LN-WX11#40****B****C LN closeup-control#10****LN closeup-WX11#40****D****E Spleen-control#10****Spleen-WX11#6****F****G Ileum-control#25****Ileum-WX11#32****H**

Figure 11

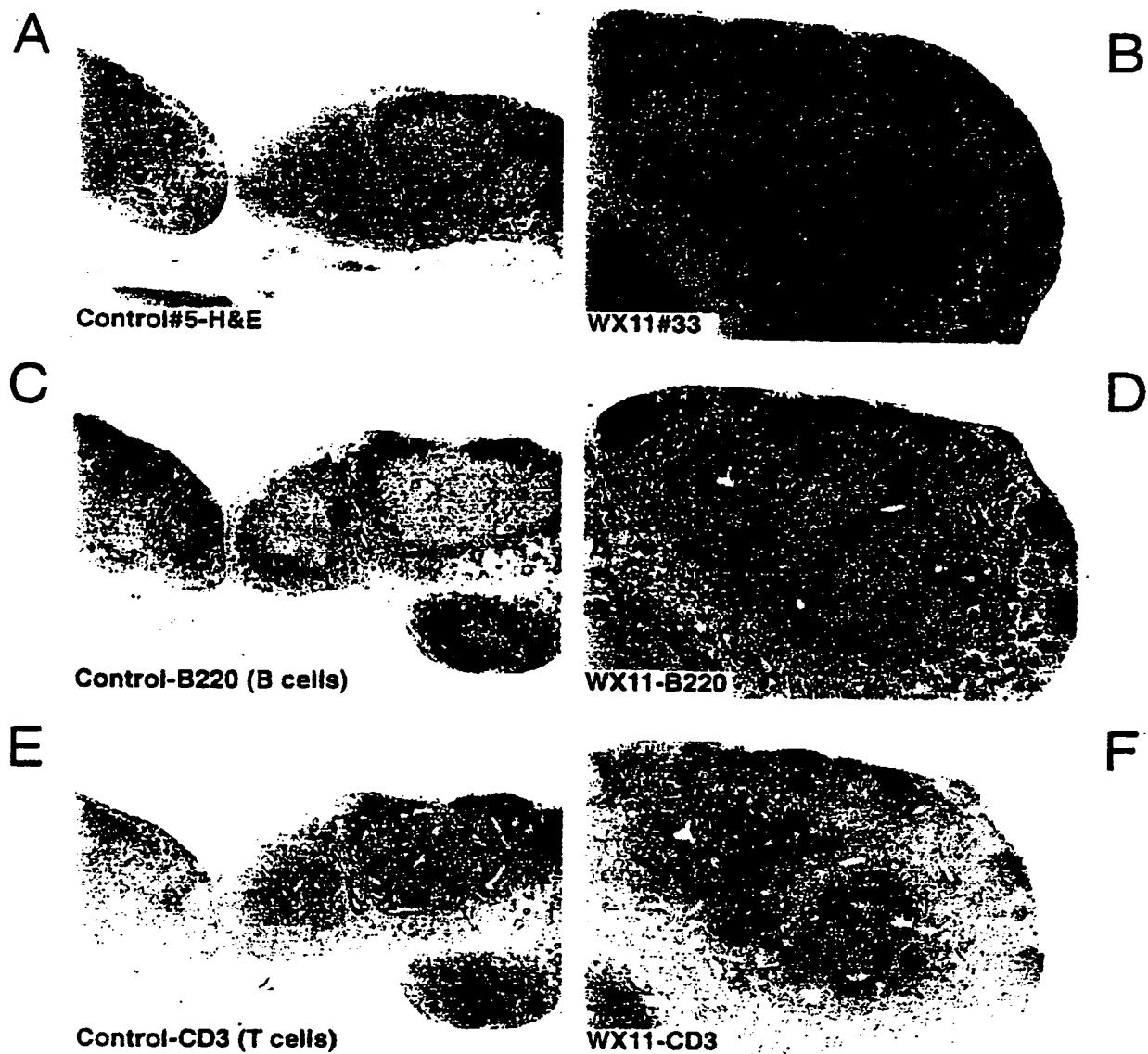


Figure 12A.

GCTGGTACGCCCTGCAGGTACCGGTCCGGAATTCCCGGGTCACCCACCGCGTCCGCCAACGCG
 TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC
 CGCGGCCCAAGTTCTCCCGCCCCGAGGTCTCCCGCCCCGAGGTCTCCGGGGGGAGGT
 CTCCGCCCGCACC -138
 -76
 -14
 -1

ATG	CGG	CTG	GGC	AGT	CCT	GGA	CTG	CTC	TTC	CTG	CTC	TTC	AGC	AGC	45
M	R	L	G	S	P	G	L	L	F	L	L	F	S	S	
															15
CTT	CGA	GCT	GAT	ACT	CAG	GAG	AAG	GAA	GTC	AGA	GCG	ATG	GTA	GGC	90
L	R	A	*D	*T	*Q	*E	K	*E	V	R	A	*M	V	G	
															30
AGC	GAC	GTG	GAG	CTC	AGC	TGC	GCT	TGC	CCT	GAA	GGA	AGC	CGT	TTT	135
S	D	V	E	L	S	C	A	C	P	E	G	S	R	F	
															45
GAT	TTA	AAT	GAT	GTT	TAC	GTA	TAT	TGG	CAA	ACC	AGT	GAG	TCG	AAA	180
D	L	N	D	V	Y	V	Y	W	Q	T	S	E	S	K	
															60
ACC	GTG	GTG	ACC	TAC	CAC	ATC	CCA	CAG	AAC	AGC	TCC	TTG	GAA	AAC	225
T	V	V	T	Y	H	I	P	Q	N	S	S	L	E	N	
															75
GTG	GAC	AGC	CGC	TAC	CGG	AAC	CGA	GCC	CTG	ATG	TCA	CCG	GCC	GGC	270
V	D	S	R	Y	R	N	R	A	L	M	S	P	A	G	
															90
ATG	CTG	CGG	GGC	GAC	TTC	TCC	CTG	CGC	TTG	TTC	AAC	GTC	ACC	CCC	315
M	L	R	G	D	F	S	L	R	L	F	N	V	T	P	
															105
CAG	GAC	GAG	CAG	AAG	TTT	CAC	TGC	CTG	GTG	TTG	AGC	CAA	TCC	CTG	360
Q	D	E	Q	K	F	H	C	L	V	L	S	Q	S	L	
															120
GGA	TTC	CAG	GAG	GTT	TTG	AGC	GTT	GAG	GTT	ACA	CTG	CAT	GTG	GCA	405
G	F	Q	E	V	L	S	V	E	V	T	L	H	V	A	
															135
GCA	AAC	TTC	AGC	GTG	CCC	GTC	GTC	AGC	GCC	CCC	CAC	AGC	CCC	TCC	450
A	N	F	S	V	P	V	V	S	A	P	H	S	P	S	
															150
CAG	GAT	GAG	CTC	ACC	TTC	ACG	TGT	ACA	TCC	ATA	AAC	GGC	TAC	CCC	495
Q	D	E	L	T	F	T	C	T	S	I	N	G	Y	P	
															165
AGG	CCC	AAC	GTG	TAC	TGG	ATC	AAT	AAG	ACG	GAC	AAC	AGC	CTG	CTG	540
R	P	N	V	Y	W	I	N	K	T	D	N	S	L	L	
															180
GAC	CAG	GCT	CTG	CAG	AAT	GAC	ACC	GTC	TTC	TTG	AAC	ATG	CGG	GGC	585
D	Q	A	L	Q	N	D	T	V	F	L	N	M	R	G	
															195
TTG	TAT	GAC	GTG	GTC	AGC	GTG	CTG	AGG	ATC	GCA	CGG	ACC	CCC	AGC	630
L	Y	D	V	V	S	V	L	R	I	A	R	T	P	S	
															205
GTG	AAC	ATT	GGC	TGC	TGC	ATA	GAG	AAC	GTG	CTT	CTG	CAG	CAG	AAC	675
V	N	I	G	C	C	I	E	N	V	L	L	Q	Q	N	
															225
215									220						

09/890729

PCT/US00/01871

WO 00/46240

19/33

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC	900
Y A G A W A V S P E T E L T G	
300	
CAC GTT TGA	909
H V STOP	
302	
CCGGAGCTCACCGCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG	971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAAGGGGAGCAGCTTGGGGCAGCCCCAGAAGGAC	1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTC	1095

TOP SECRET//NOFORN

09/890729

PCT/US00/01871

WO 00/46240

20/33

Figure 12B.

human	MRLGSP-----	G L-LF-LLFSS LRADTQEKEV	25
mouse	MQLKCPFCVS LGTRQPWKK LHVSSGFFSG LGLFLLLLSS LCAASAETEV	50	
Consensus	M.L..P..... G L.LF.LL.SS L.A...E.EV	50	
human	RAMVGSDVEL SCACPEGSRF DLNDVYVYWQ TSESKTVVTY HIPQNSSLLEN	75	
mouse	GAMVGSNVVL SCIDPHRRHF NLSGLYVYWQ IENPEVSVTY YLPYKSPGIN	100	
Consensus	.AMVGS.V.L SC..P....F .L...YVYWQ VTY ..P..S...N	100	
human	VDSRYRNRAL MSPAGMLRGD FSLRLFNVT P QDEQKFHCLV LSQ-SLGQFQE	124	
mouse	VDSSSYKNRGH LSLDSMKQGN FSPLYLKVNT P QDTQEFTCRV FMNTATELVK	150	
Consensus	VDS.Y.NR.. .S...M..G. FSL.L.NVT P QD.Q.F.C.V	150	
human	VLSVEVTLHV AANFSVPVVS APHSPSQ-DE LTFTCTSING YPRPNVYWIN	173	
mouse	ILEEVVRLRV AANFSTPVIS TSDSSNPGQE RTYTCMSKNG YPEPNLYWIN	200	
Consensus	.L...V.L.V AANFS.PV.S ...S.....E .T.TC.S.NG YP.PN.YWIN	200	
human	KTDNSLLDQA LQNDTVFLNM RGLYDVSVL RIARTPSVNI GCCIENVLLQ	223	
mouse	TTDNSLIDTA LQNNNTVYLNK LGLYDVI STL RLPWTSRGDV LCCVENVALH	250	
Consensus	.TDNSL.D.A LQN.TV.LN. .GLYDV.S.L R...T..... .CC.ENV.L.	250	
human	QNLTVGQSQTG NDIGERDKIT ENPVSTGEKN AATWSILAVL CLLVVVAVAI	273	
mouse	QNITSISQAE SFTGNNTKNP QETHNNELKV LV--PVLAVL AAAAFVSFII	298	
Consensus	QN.T..SQ..G...K..K.LAVLV...I	300	
human	GWVCRDRCLQ HSYAGAWAVS PETELTGHV	302	
mouse	YR--RTR-PH RSYTGPKTVQ LE--LTDHA	322	
ConsensusR.R... .SY.G...V. .E..LT.H.	329	

Figure 13A

AACAAATTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA - 111
 CTCACTATAGGGAAAGCTGGTACGCCCTGCAGGTACCGTCCGGATTCCGGGTC - 56
 GACCCACCGCGTCCGTAAACACTGAACCGCAGGACTGTTAACTGTTCTGGCAAAC - 1

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT 45			
M K S G L W Y F F L F C L R I			
5	10	15	
AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90			
<u>K V L T</u> *G *E I N G S A N Y E M			
20	25	30	
TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT 135			
F I F H N G G V Q I L C K Y P			
35	40	45	
GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 180			
D I V Q F K M Q L L K G G Q			
50	55	60	
ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG 225			
I L C D L T K T K G S G N T V			
65	70	75	
TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 270			
S I K S L K F C H S Q L S N N			
80	85	90	
AGT GTC TCT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC 315			
S V S F F L Y N L D H S H A N			
95	100	105	
TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA 360			
Y Y F C N L S I F D P P P F K			
110	115	120	
GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT 405			
V T L T G G Y L H I Y E S Q L			
125	130	135	
TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT 450			
C C Q L K F W L P I G C A A F			
140	145	150	
GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA 495			
V V V C I L G C I L I C W L T			
155	160	165	
AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540			
K K K Y S S V H D P N G E Y			
170	175	180	
ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585			
M F M R A V N T A K K S R L T			
185	190	195	
GAT GTG ACC CTA TAA 600			
D V T L STOP			
199			
TATGGAACCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTCTCAACTTGA 655			
AGTGCAAGATTCTCTTATTCGGGACCACGGAGAGTCTGACTAACATACA 710			

09/890729

PCT/US00/01871

WO 00/46240

22/33

TCTTCTGCTGGTGTTCATCTGGAAGAACGACTGTATCAGTCAATGGGGAA	765
TTTTAACAGACTGCCTGGTACTGCCAGTCCTCTCAAAACAAACACCCTTGC	820
AACCAGCTTGAGAAAGCCCAGCTCTGTGCTACTGGGAGTGGAAATCCCTG	875
TCTCCACATCTGCTCTAGCAGTCAGCCAGTAAAACAAACACATTACAAG	930
AAAAATGTTAAAGATGCCAGGGGTAUTGAATCTGAAAGCAAATGAGCAGCCA	985
AGGACCAGCATCTGTCGCAATTCACTATCATACTACCTCTTCTGTAGGGA	1040
TGAGAATTCCCTTTAATCAGTCAAGGGAGATGCTCAAAGCTGGAGCTATTT	1095
ATTTCTGAGATGTTGATGTGAACGTACATTAGTACATACTCAGTACTCTCCTTC	1150
AATTGCTGAACCCAGTTGACCATTACCAAGACTTAGATGCTTCTGTGCC	1205

Figure 13B

hCRP1	MKSGLWYFFLFCLRIKVLTGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLTKTKGSGNTVSIAKSLKFCHSQLSNNSVSSFLYNLD	100
mCRP1	LKMRLFREREVLCELTKTKGSGNAVSIKNPMLCLYHLSNNSVSSFLNNPD	100
hCRP1	HSHANYYFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPIGCAA	149
mCRP1	SSQGSYYFCSLISIFDPPPFQERNLSSGGYLHIYESQLCCQLKLWLPVGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTI	199
mCRP1	FVVVLLFGCILIIWFSKKKYGSVHDPNSEYMFMAAVNTNKKSRLAGVTS	200

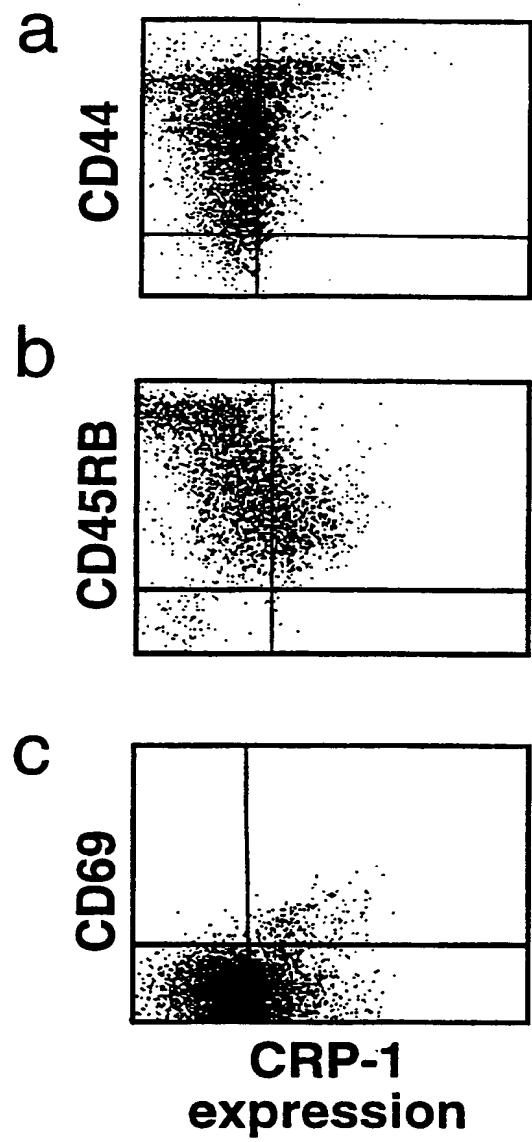
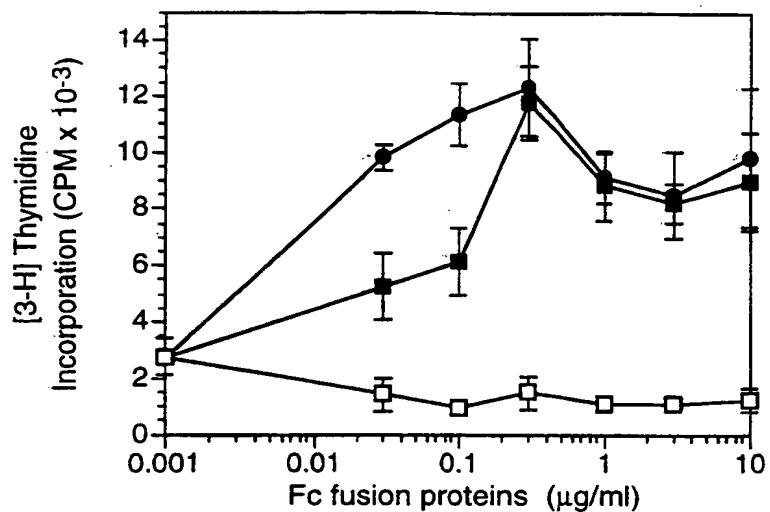
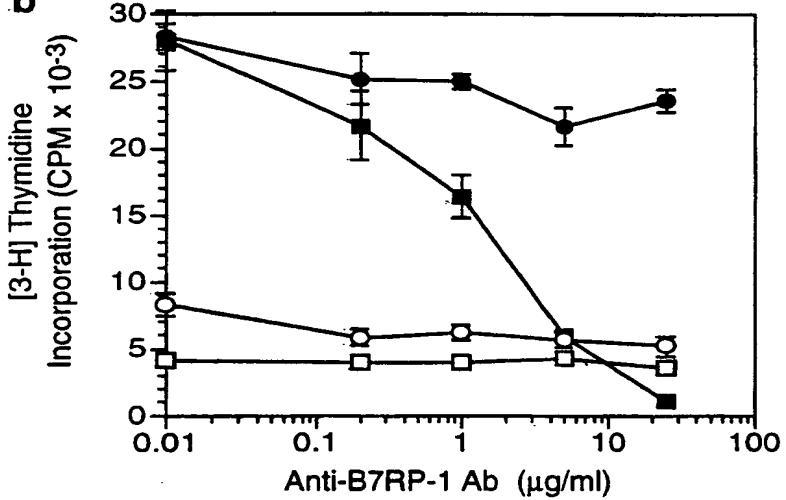
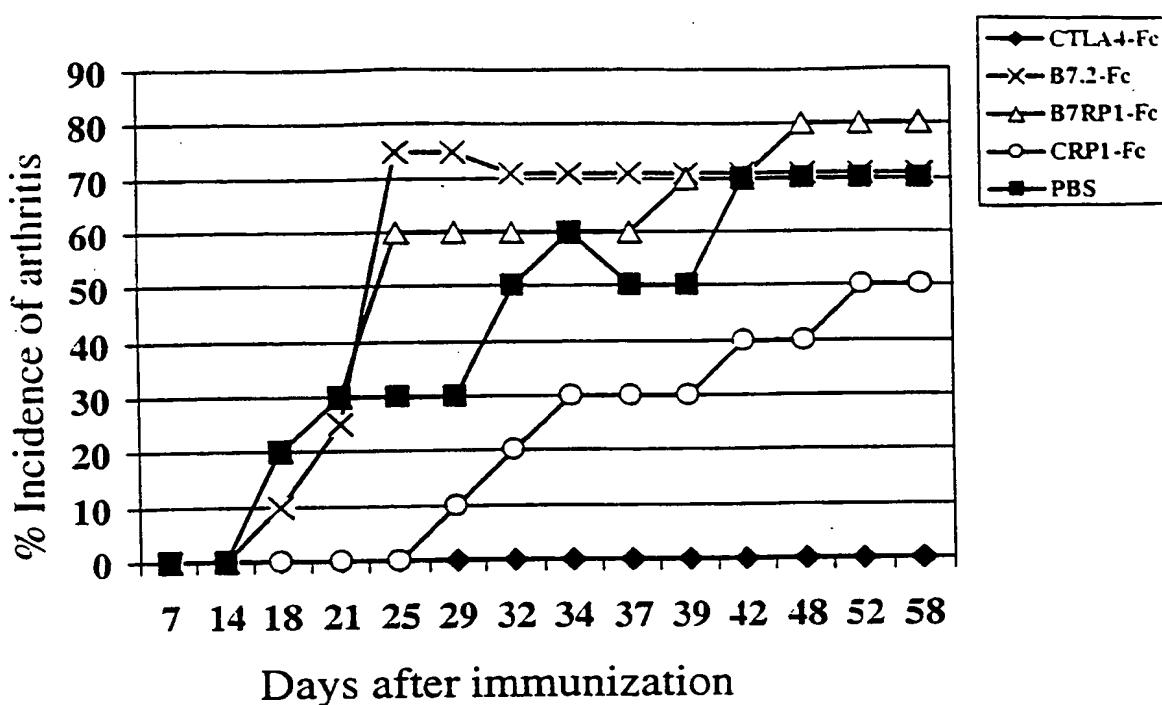


Figure 14

a**b****Figure 15**

26/33

A.



B.

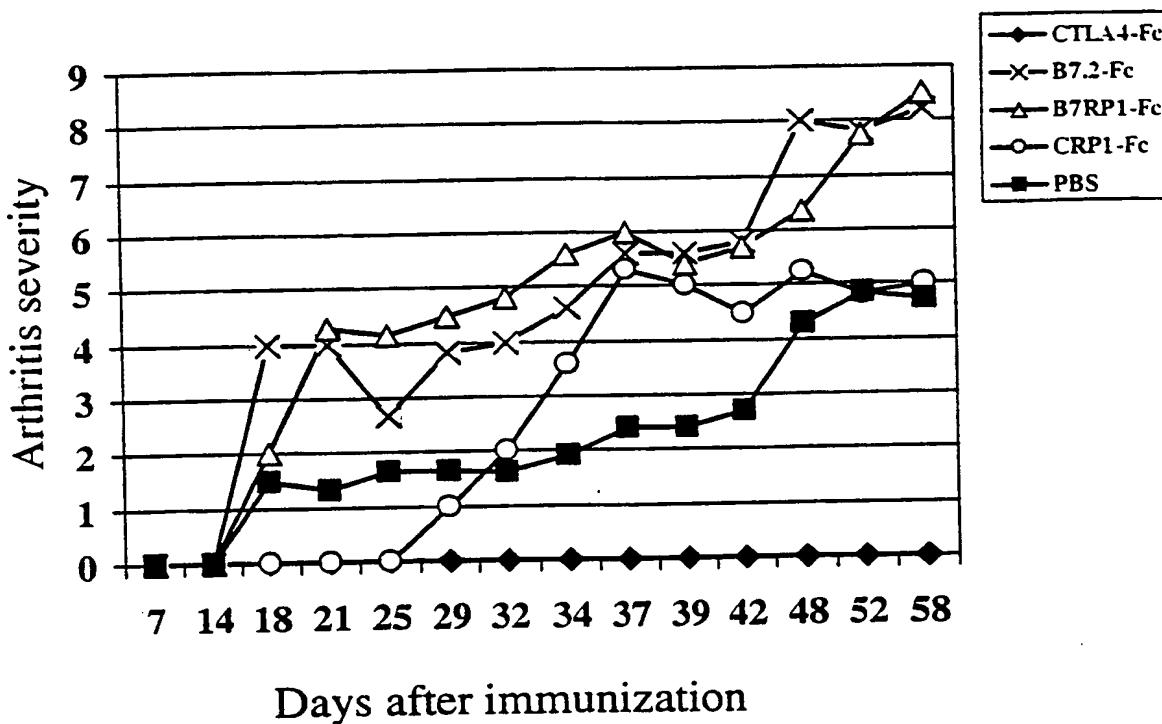


Figure 16

Figure 20

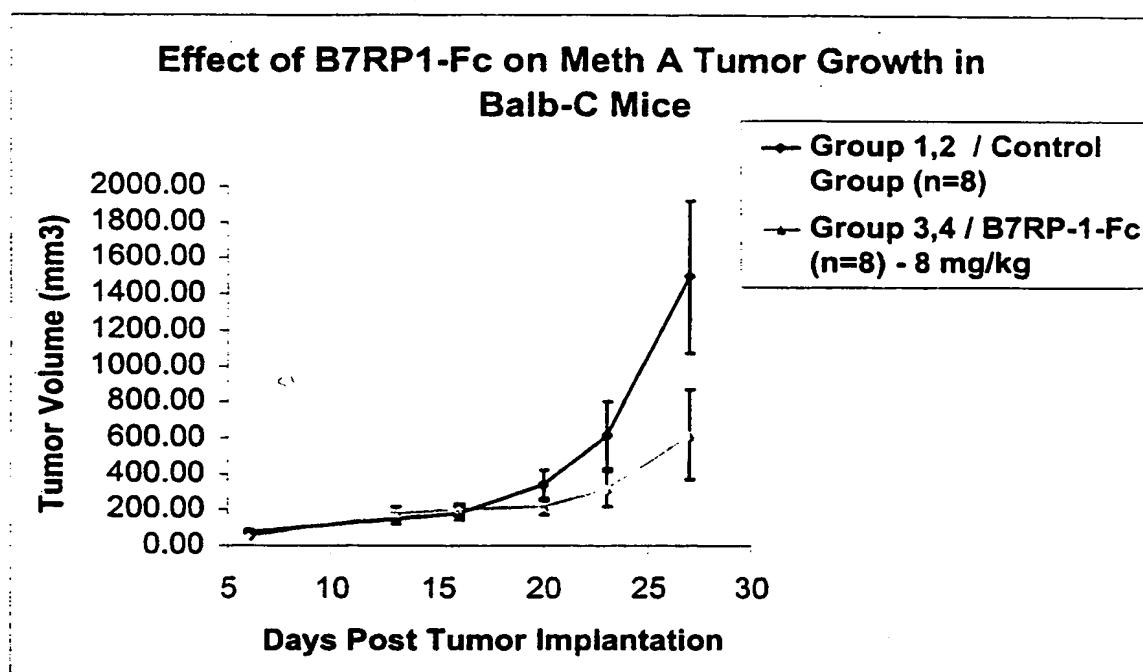


Figure 21A/B.

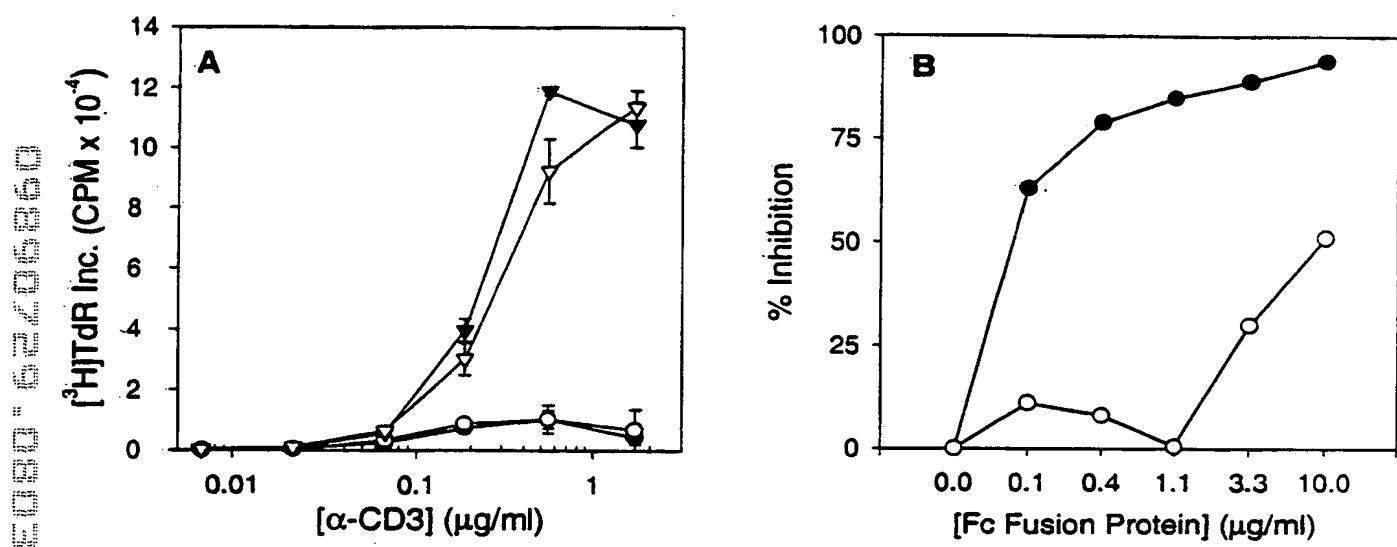


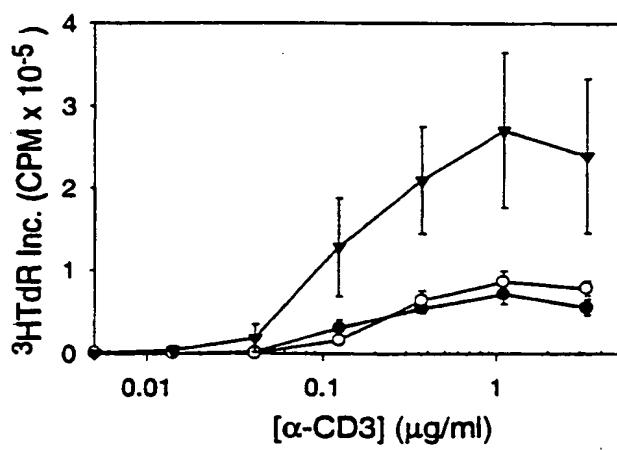
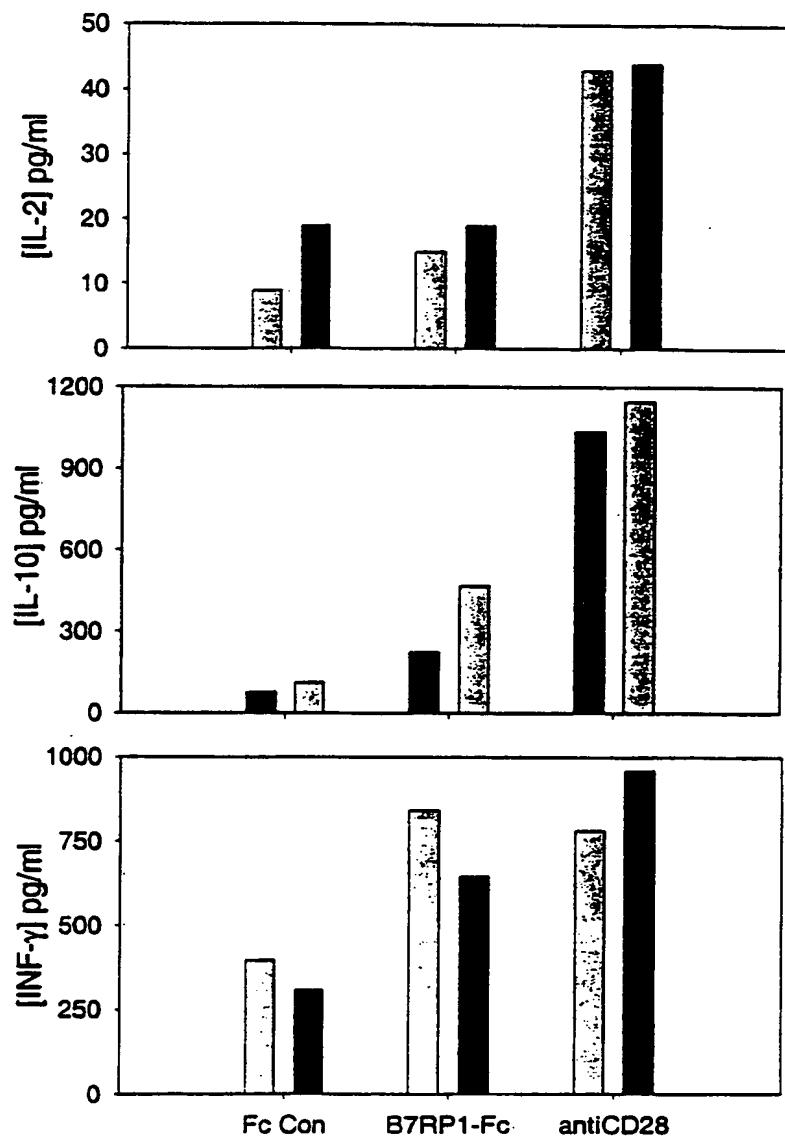
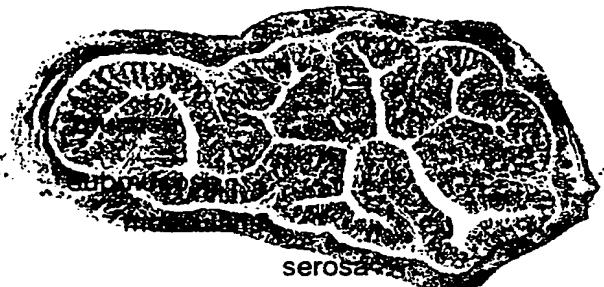
Figure 21C.

Figure 21D



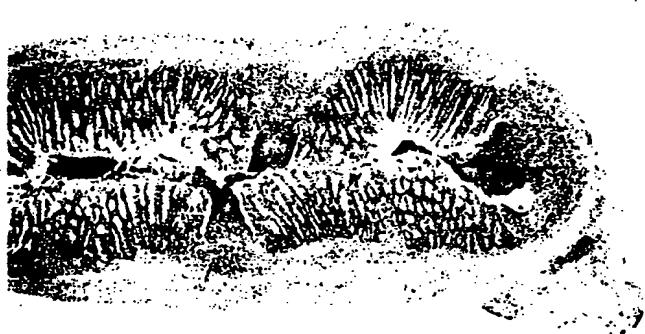
PCT/US 00 '01871



A. Control mouse#53F:Prox. colon 40X



B. Mouse#111F:Prox. colon 40X



C. Mouse#111F: Prox. colon 20X



D. Mouse#111F: closeup of mucosa 100X

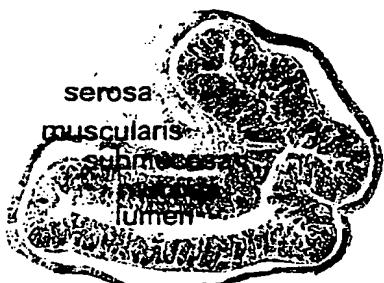


E. Mouse#112F: Giant cell, submucosa

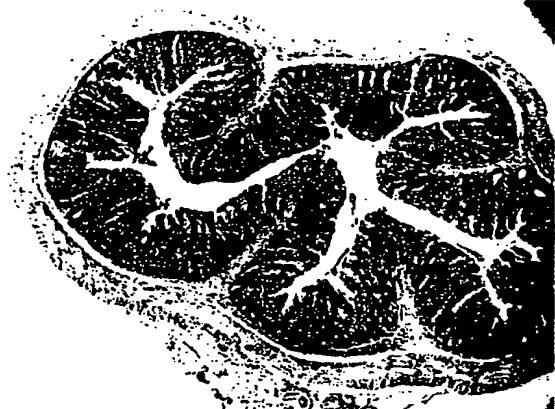


F. Mouse#112F:epithelioid macrophages

Figure 17



A. Control mouse#53F:Distal colon, 40X



B. mouse#111F:Distal colitis, 40X



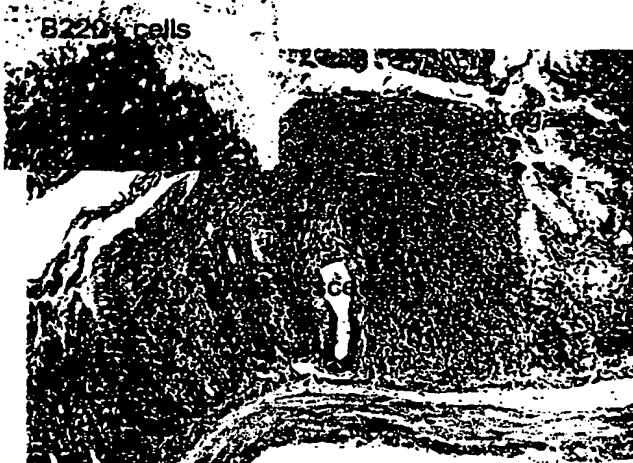
C. mouse#55M:Distal colitis, 40X



D. mouse#112F:Distal colon, 40X

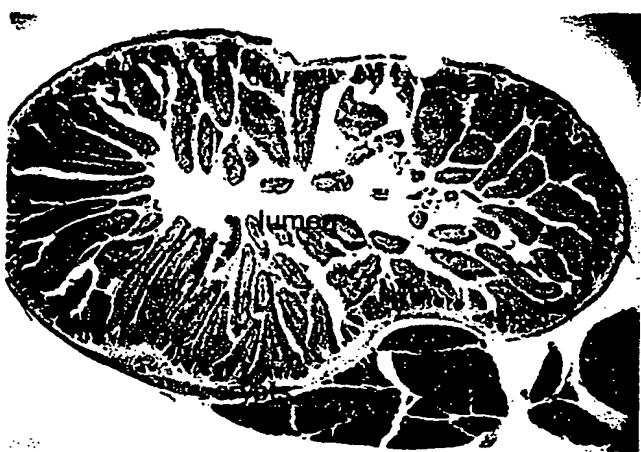


E. mouse#112:CD3+ T-cells, 40X

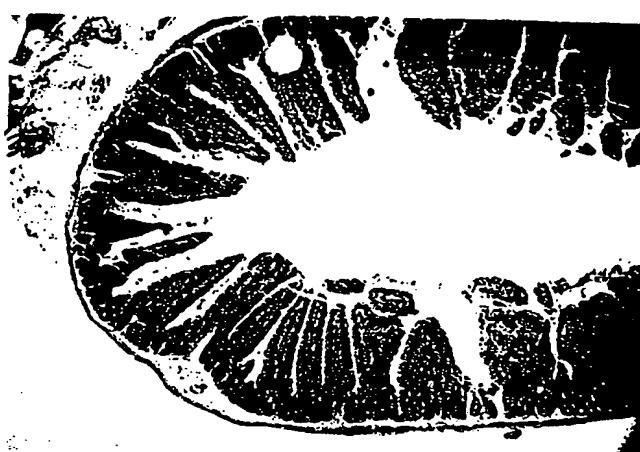


F. mouse#112:closeup, 100X

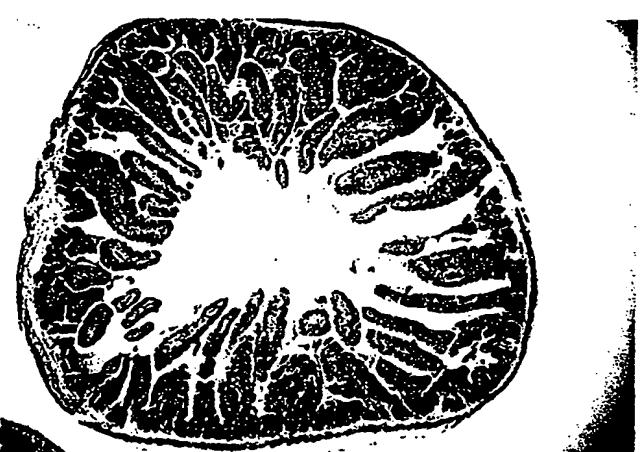
Figure 18



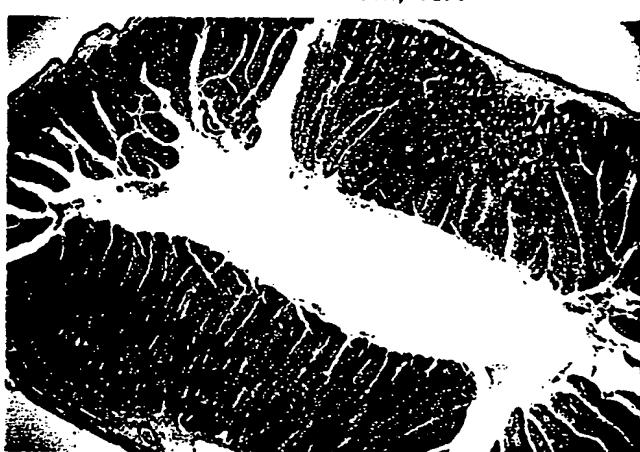
A. Control mouse#53F:duodenum, 40X



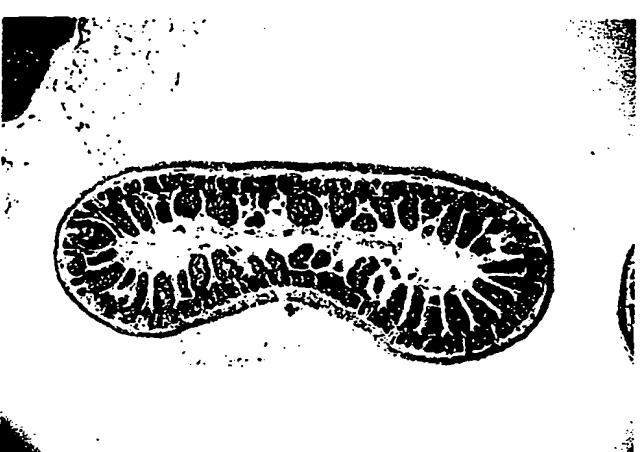
B. Mouse#51F:duodenum, 40X



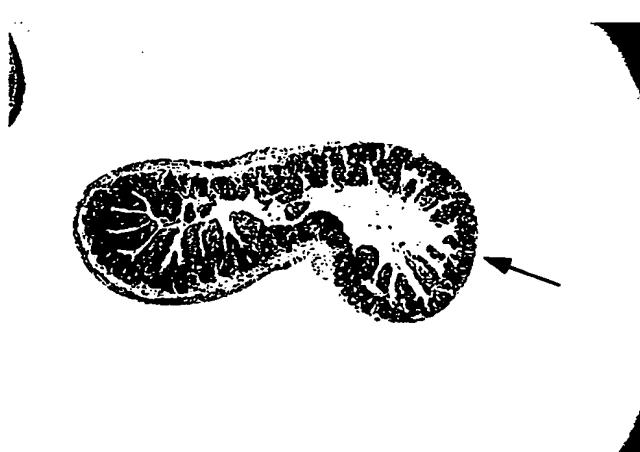
C. Control mouse#53F:jejunum, 40X



D. Mouse#51F:jejunal hyperplasia, 40X



E. Control mouse#53F:ileum, 40X



F. Mouse#231M:ileal atrophy, 40X

Figure 19